


```
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 43200
;; LENGTH: 68
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC005037.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.69
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.4
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.89
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1
;; OTHER INFORMATION: EST_HUMAN HIT: BE275324.1, EVALUATE 4.00e-35
;; OTHER INFORMATION: SWISSPROT HIT: P54472, EVALUATE 1.00e-10
US-09-745-506-74 (1-1553) x US-09-864-761-43200 (1-68)
Alignment Scores:
Pred. No.: 1,54e-27 Length: 68
Score: 366.00 Matches: 68
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.12% Indels: 0
Gaps: 0
US-09-745-506-74 (1-1553) x US-09-864-761-43200 (1-68)
QY 395 ATGGAGAGAGTGTGCGAAAGAGGAGACCTATTCTCTCCATCCGCTATCTTC 454
D 1 MetGluIuValLeuGlnLysAlaAspLeuIleuSerYrHisProIlePhe 20
QY 455 CGAACCCATGAAGGCATACCTGGAACACATGGAAGAGAGCGCTGATCCGGGCTGTG 514
D 21 ArpPrometLysArgIleThrPheSerThrTrpLysGluArgLeuValIleArgAlaLeu 40
QY 515 GAGAACAGAGTGTGATCTACTCTCTCATACAGCCATGATGCTGCGCCCAAGGCGTC 574
D 41 GluAsnArgValGlyIleTyrSerProHisThrAlaTyrAspAlaIleProGlnGlyVal 60
QY 575 AACAACTGCTGGCTAAAGGCTT 598
D 61 AsnAsnTrpLeuAlaLysGlyLeu 68
RESULT 2
US-09-738-626-5952
; Sequence 5952, Application US/09738626
```

```
;; Publication No. US20020197605A1
;; GENERAL INFORMATION:
;; APPLICANT: NAKAGAWA, SATOSHI
;; APPLICANT: MIZOGUCHI, HIROSHI
;; APPLICANT: ANDO, SEIKO
;; APPLICANT: HAYASHI, MIKIRO
;; APPLICANT: OCHIALI, KEIKO
;; APPLICANT: YOKOI, HARUHIKO
;; APPLICANT: TATEISHI, NAOKO
;; APPLICANT: SENOH, AKIHITO
;; APPLICANT: IKEDA, MASATO
;; APPLICANT: OZAKI, AKIO
;; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
;; FILE REFERENCE: 249-125
;; CURRENT APPLICATION NUMBER: US/09/738,626
;; CURRENT FILING DATE: 2000-12-18
;; PRIOR APPLICATION NUMBER: JP 99/377484
;; PRIOR FILING DATE: 1999-12-16
;; PRIOR APPLICATION NUMBER: JP 00/159162
;; PRIOR FILING DATE: 2000-04-07
;; PRIOR APPLICATION NUMBER: JP 00/280988
;; PRIOR FILING DATE: 2000-08-03
;; NUMBER OF SEQ ID NOS: 7059
;; SOFTWARE: PatentIn ver. 3.0
;; SEQ ID NO 5952
;; LENGTH: 380
;; TYPE: PRT
;; ORGANISM: Corynebacterium glutamicum
US-09-745-506-74 (1-1553) x US-09-738-626-5952 (1-380)
Alignment Scores:
Pred. No.: 1,09e-13 Length: 380
Score: 230.00 Matches: 89
Percent Similarity: 44.35% Conservative: 72
Best Local Similarity: 24.52% Mismatches: 154
Query Match: 8.25% Indels: 48
Gaps: 13
US-09-745-506-74 (1-1553) x US-09-738-626-5952 (1-380)
QY 293 TCGTTTGTGAGATGGAGCAATGTGGATTACTGTGGAAACCAACCCACATCACT 352
D 20 AlaLeuAlaGluSerThrPheArgLysValGlyLeuIleCys---GlyAspProThrGluSer 38
QY 353 GTAAATACACTCTTCCTGACCAATGACCTGACAGGAAGTATGAGAGAGTGTGCAA 412
D 39 ValLysArgValGlyLeuAlaLeuAspCysThrGlnAlaValAlaAspLysAlaValAsp 58
QY 413 AAGAAGCAGACCCATCTCTCTACCATCCGCTATCTTCGACCCATGAGACGCATA 472
D 59 MetGlyLeuAspMetLeuIleIleHisThrLeuLeuLeuArgGlyValThrSerVal 78
QY 473 ACCTGGAACACATGGAAGAGCGCTGTGATCCGGCTGTGGAACAGAGTCGTATC 532
D 79 AlaAlaAspGluPheProLysGlyLysValIleHisThrLeuIleArgGlyValAlaLeu 98
QY 533 TACTCTGCTACACGCTATGATCTGCGCCCGAGGCGTCAACAACATGTTGGCTAA 592
D 99 PheSerGlnHisThrAsnAlaAspSerAlaArgProGlyValAsnAspLysLeuAlaGlu 118
QY 593 GGGCTTGAGCTGTACTCTCCAGGCCATGACATCTTCCAAAGCTCCCAACTACCTTACA 652
D 119 LeuValAlaLysIleThrAlaGlyArgProIleAlaThrArgLeuLeuGlyGlyMetAspLys 138
QY 653 GAGGGAACACAGAGAGATTCATCAAGTAACTACACACCAAGACGCG-----GACAAA 706
D 139 TrpGlyValHisValLeuProLysAspAlaAlaTyrLeuLysMetLeuPheAspAla 158
QY 707 GTCATGCTGCAGTGAAGA-----ATTGACGGTGTGTTCT--- 742
D 159 GlyAlaGlyAlaIleGlyAspTyrArgGluCysAlaPheGluIleGlyGlyThrGlyGln 178
QY 743 -----GTCACTTCTTTTCTGCTAGACGTGTAATAGAGAACAAACAGCATTAAT 793
```

```

Db      179 pheargProvalGluLylalaenProAlaGluLylAspValAspLys----- 194
QY      794 CTGAATTGTACTCAGAGCGTTTGTATCAGAGGTAGATTTCTTCCCGGAAACAACA 853
Db      195 -----LeuphlysserLeuLylLeuArgLlGluPhValAlaProArgAsnLeu 211
QY      854 CTTTATCAGAGCGAATTCG-----TCACTGGAGAAAGCTTTGCTT--- 898
Db      212 ArgAlaArgLeuThrSerValLeuArgGluAlaHisProTyrGluGluProAlaPheAsp 231
QY      899 -----CTACAT-----ACTGAATGGAGCGTTATGC 925
Db      232 lIeValGluMetHisSerAlaGluSerLeuGluAsnAlaThrGlyLeuGlyAlaGly 251
QY      926 ACACGTGATGATCTCTCCCTGCGAACCATGATTGATGAAATAAAGACACTAAA 985
Db      252 GluLeuProGluProMetArgLeuAlaAspPheValGluGluValAlaAsnAsnLeuPro 271
QY      986 CTATCTCATATTCGTTAGCCCTTGGGGGGGAGAAC-----TTAGATCTCAATGC 1039
Db      272 ValThrGlu-----TrrGlyValArgAlaThrGlyAspProGluGluMetVal 287
QY      1040 AAAGTCGTGAGCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1090
Db      288 SerArgValAlaValIserSerGlySerGlyAspSerPheLeuAsnAspValIleGlyLeu 307
QY      1091 GAGCGTACCTTACTCTCAGAGTGTGAGATGCCATCATGATCTTTGGATGCTGCTTCC 1150
Db      308 GlyValAlaValIleThrSerAspLeuArgHisIleProValAspGluTyrLeuArg 327
QY      1151 CAATTAATGATCTCATCTCTGTGAGACAGACAGAACAGAGCGTTCTTCTTCT 1207
Db      328 GluGlyGlyProAlaValIleAspThrAlaHisTrrAlaSerGluPheProThrSer 347
QY      1208 GACCTTCGAGATATGCTG---GATTCCTACCTTGAGATTAATTAATTAATTAATTA 1264
Db      348 GluAlaGluGluIleLeuGluAsnAspLysAlaProGluValGluValAspValIleSerIle 367
QY      1265 GAGACTGCAC 1273
Db      368 ArgThrAsp 370

RESULT 3
US-10-156-761-13402
; Sequence 13402, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ. ID NOS: 15109
; SEQ. ID NO 13402
; LENGTH: 287
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-13402

Alignment Scores:
Pred. No.: 1,31e-12 Length: 287
Score: 218.50 Matches: 79

```

```

Percent Similarity: 34.63% Conservative: 46
Best Local Similarity: 21.88% Mismatches: 125
Query Match: 7.83% Gaps: 111
DB: 15

US-09-745-506-74 (1-1553) x US-10-156-761-13402 (1-287)

QY      251 TTGAAGGCTCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 310
Db      4 LeuSerGluValAlaIleAlaIleLeuGluAsnLeuThrProAlaGluThrAlaGluSerThr 23
QY      311 GACAAATGTTGATTAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 370
Db      24 AspAlaValAlaGlyThrValValAlaGlyAspProAspGluGluValAlaAlaGlyLeuPheAla 43
QY      371 ACCAATGACCTGACTGAGAGTGTAGTGGAGAGGTGTGTGTGTGTGTGTGTGTGTGTGT 430
Db      44 Val---AspProValArgGluIleValAspGluValAlaHisLeuGlyAlaAspLeuLeu 62
QY      431 CTCTCTACATCCGCTATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 490
Db      63 ValThrHisIleProLeuTyrLeuArgGlyThrThrValAlaAlaIleSerThrPheLys 82
QY      491 GAGCGCTGTGTATCCGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 550
Db      83 GlyArgValAlaHisThrLeuIleLysAsnAspIleAlaLeuHisValAlaHisThrAsn 102
QY      551 TATGATCTCTCGCCCGGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 610
Db      103 AlaAspArgAlaAspProGlyValSerAspAlaLeuAlaGlyAlaLeuAspLeuArgVal 122
QY      611 TCCAGCGCCATACATCTTCCAAAGCTCCCAAGCTTCAAGCTTCAAGCTTCAAGCTTCAAG 670
Db      123 ValArgProLeuValProAsp---ProGlyAspPro----- 133
QY      671 GAATTCACGTTAATCTACACCAAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 730
Db      133 ----- 133
QY      731 GAGCGTCTTCTGTCTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 790
Db      134 AspGly----- 135
QY      791 AATCTGAATGTACTCAGAAAGCTTGTATGACAGTGTGTGTGTGTGTGTGTGTGTGTGT 850
Db      135 ----- 135
QY      851 CAATTTATCAGAGAGCGAATTTCTGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 910
Db      136 -----ArgArgGly 138
QY      911 ATGGAGCGTTATGACACATGATGATCTGTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGT 970
Db      139 LeuGlyArgValCysAlaLeuAspHisProValThrValArgGluPheAlaAlaArgAla 158
QY      971 AAAAGACCTTAATAATCTCATATTCGTTAGCCCTTGGGGGGGAGAGAACTTGTAGAG 1030
Db      159 AlaAlaArgLeuProAlaThr-----AlaGluGlyLeuArgValAlaGlyAspProGlu 176
QY      1031 TCTCAAGTCAAAAGTGTGCGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1090
Db      177 AlaLeuValArgThrValAlaValIserGlyGlySerGlyAspSerLeuPheAspAspVal 196
QY      1091 GAGGCT-----GACCTTACTCTACAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1135
Db      197 ArgAlaAlaGlyValAspAlaPheLeuThrAlaAspLeuArgHisIleHisProAlaSerGlu 216
QY      1136 -----TTGATGCTGTGTCTCCCAAGGATA 1159
Db      217 PheMetAlaAspArgAlaHisSerProLeuAlaLeuLeuAspAlaAlaHisTrrAlaThr 236
QY      1160 AATGTCACTCTGTGTGAACAGCAAGCACTGAAGAGAGCTTCTTCTTCTGACCTTGTGAGAT 1219

```

Db 237 GluTrpProTrpCysGluLeuAlaAlaGlnLeuAspGluIleSerAspArgHisGly 256
QY 1220 ATGCTGATTCCTCACTTGAGAGATTAATAATATTAATCCATACAGAGACTGAGAGGAC 1279
Db 257 Trp-----AspLeuArgValHisValSerIsthrValThrAsp 269
QY 1280 CCT 1282
Db 270 Pro 270
RESULT 4
US-08-808-031A-45
; Sequence 45, Application US/08808031A
; Publication No. US20020048802A1
; GENERAL INFORMATION:
; APPLICANT: Inouye, Sumiko
; APPLICANT: Hsu, Mei-Yin
; APPLICANT: Eagle, Susan
; APPLICANT: Inouye, Masayori
; TITLE OF INVENTION: PROKARYOTIC REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WEISER & ASSOCIATES
; STREET: 230 South Fifteenth Street, Suite 500
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/808,031A
; FILING DATE: 03-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Weiser, Gerard J.
; REGISTRATION NUMBER: 19,763
; REFERENCE/DOCKET NUMBER: 377(913).5888P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-875-8383
; TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 45:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 316 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-808-031A-45
Alignment Scores:
Pred. No.: 0.00899 Length: 316
Score: 119.50 Matches: 80
Percent Similarity: 35.71% Conservative: 55
Best Local Similarity: 21.16% Mismatches: 116
Query Match: 4.28% Indels: 127
Gaps: 20
US-09-745-506-74 (1-1553) x US-08-808-031A-45 (1-316)
QY 368 CTGACCAATGACCTGACTGAGGAAGTGTGAG-----GAG 403
Db 13 MetThrLysGlyPheAlaSerGluValMetArgSerProGluProIleLysIsthrAsp 32
QY 404 GTGCTGCAAAAGAGAGGACGACCTCATTTCTCTCAACATTCGCGCTATCTCCGACCATG 463
Db 33 IleAlaLysLysGlyGlyMetArgThrIleLysIsthrPro-----46
QY 464 AAGCGCATTAACCTGGAACACATGGAAGAGCGCCCTGGTGATCCGGCTCTGTGAGAACAGA 523
::: ||| ::::::::::: ||| |||

Db 47 -----SerSerLysValLysLeuIleGlnIsthrPheLeuMetAsnAsn 60
QY 524 GTCCGATTCATCTCTCTCATACAGACCTATGATGCTGGCCCGAGGGGTCACAACTGG 583
Db 61 Val-----PheSerLysLeuProMetHisnAlaLysValPheValLysAsnArg 78
QY 584 TTGGCTAAAGGGCTTGAGCTTGTAACCTCCAGGCCATACATCTCTCCAAAGCTCCCAAC 643
Db 79 SerIleLys-----SerAsnAlaLeuHisAlaGluSerLysAsnLys 93
QY 644 TAC-----CCT-----649
Db 94 TyrTrpValLysLysLeuPheLysAspPheProSerIleLysPheThrAspPheGlu 113
QY 650 -----ACAGAGGAGAAACACCGAGTAGAATTCACGTTAACTACACCCAGACCTG 700
Db 114 TyrAlaPheThrArgTyrArgAspArgLysGluPheThrIsthrGluTyrAspLysGluLeu 133
QY 701 GACAAAGTCATGTGTCAGTGAAGAAATTGACGGTGTCTT-----742
Db 134 -----LeuGlnLeuIleLysThrIleCysPheIleSerAspSerThrLeuProIle 150
QY 743 -----GTCACTCTTTTCTGCTAGACGCTGTAATGAGGAACA 781
Db 151 GlyPheProThrSerProLeuIleAlaAsnPheValAlaArgLysLeuAspLeuLys 169
QY 782 ACACGGATTAACTGAATTTACTCAGAGGCTTTGATGAGGTGATATTTCTTCC 841
Db 170 -----LeuThrGlnLys-----LeuAsnAlaIleAspLysLeuAsn 181
QY 842 CGGAACAAACACTTTATCAGACAGGAAATTCGTGACTGAGAACCTTGTCTTGA 901
Db 182 AlaThrTyrThrArgTyrAlaAspAspIleLeuValSerThrAsnMet-----197
QY 902 CATACTGGAAGGAGCGGTATGACACTGATGATGATGCTCTCCGCAACCATGAT 961
Db 198 --LysGlyAlaSerLysLeu-----IleLeu 205
QY 962 GATCGAATMAAAGACACCTAAACTATGATATTCGTTAGCCCTTGAGGTGGGAGA 1021
Db 206 AspCysPheLysArgThrMetLys-----GluIleGlyPro 217
QY 1022 ACCTTAGAGTCTCAAGTCAAGTCAAGTCTGGCCCTGTGCTGTGCTGGAGAGC---GTT 1078
Db 218 AspPheLysIleAsnIleLysLysPheLysIleCysSerAlaSerGlyLysIsthrVal 237
QY 1079 CTGCAGGCTGTGAGGCT-----GACCTTAACCTCAGAGGTGAGATGTCATCATGAT 1132
Db 238 ValThrGlyLeuLysValCysHisAspPheHisIleThrLeuHisArgSerMetLysAsp 257
QY 1133 ACT-----TTGGATGCTGCTTCCCAAGGAATTAATGTCATGCTCTGTGACAC 1180
Db 258 LysIleArgLeuHisIleSerLeuSerLysGlyIle-----LeuLysAspLeuLys 275
QY 1181 AGCAGACTGAAGAGCGGTTCTTCTGACCTCAGATATGATGATTCACATCTGGAG 1240
Db 276 HisAsnLysLeuSerGlyTyrIleAlaTyrAlaLysAsp-----IleAspProHisPheYr 294
QY 1241 AATAAGTAATAATTAATTCCTATCAGAGACTGACAGGACCCCTTCAGGTGGTAAATG 1300
Db 295 ThrLysLeuAsn-----298
QY 1301 CAGAAATCATCAGATACACATCTCTACAAATCAGCTGAGGCCAATTAAT 1354
Db 299 ArgLysTyr-----PheGlnGlnIleLysTyrPheGlnAsnLeuHis 312
RESULT 5
US-10-136-761-7961
; Sequence 7961, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OKURA, SATOSHI
; APPLICANT: IKEDA, HARO

```

: APPLICANT: ISHIKAWA, JUN
: APPLICANT: HORIKAWA, HIROSHI
: APPLICANT: SHIBA, TADAYOSHI
: APPLICANT: SAKAKI, YOSHIYUKI
: APPLICANT: HATTORI, MASAHIRA
: TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
: FILE REFERENCE: 249-262
: CURRENT APPLICATION NUMBER: US/10/156,761
: CURRENT FILING DATE: 2002-05-29
: PRIOR APPLICATION NUMBER: JP 2001-204089
: PRIOR FILING DATE: 2001-05-30
: PRIOR APPLICATION NUMBER: JP 2001-272697
: NUMBER OF SEQ ID NOS: 15109
: SEQ ID NO 7961
: LENGTH: 3352
: TYPE: PRT
: ORGANISM: Streptomyces avermitilis
US-10-156-761-7961

```

```

Alignment Scores:
Pred. No.: 0.616      Length: 3352
Score: 106.00      Matches: 91
Percent Similarity: 34.94%      Conservative: 34
Best Local Similarity: 21.93%      Mismatches: 144
Query Match: 3.80%      Indels: 126
DB: 15      Gaps: 18

```

US-09-745-506-74 (1-1553) x US-10-156-761-7961 (1-3352)

```

QY 309 GGGACAAATGTTGAT-----TACTGGTGAACCAAGCCACAC 347
DB 2295 GYTHrValLeuAsprhThrThrLeuAspAlaGluTyrTrpYrAlaGlnHis 2314
QY 348 ATACGTAATAC-----ACTCTCTGACCAATGACCTGACGAGAG 392
DB 2315 ThrVal-GluPheGluTrpThrValArGthrLeu-----A 2327
QY 393 TGATGAGAGAGGTGTGCAAAAGAGCCATCTCTCTCCATCCGCTATCT 452
DB 2327 AsprGlnHisGluValPheValGluCysSerProHisProLeuAlaAspAlaValG 2347
QY 453 TCCGACCCATGAAGCCATACCTCGACACACATGGAAGAGCGCTGATCCGGCTC 512
DB 2347 nGluIleAlaGluGluThrGlyAlaAspAlaValThrGlySerSerLeuArGArgGlyG 2367
QY 513 TGGAGAACAGACTCGTATCTA-----CTCCCTCATACAG 534
DB 2367 nGlyGluMetAspArgPheLeuArgSerValSerGluLeuHisValSerGlyValHisVa 2387
QY 535 -----CTCCCTCATACAG 548
DB 2387 LaspleuthrAlaProPheAlaGlyArGProValArGArgValAspLeuProThrTyr-A 2407
QY 549 CCTAT-----GATGCTGCGCCCAAGCGGCTAC- 577
DB 2407 LaPheGlnProGlnArGlyTyrTrpLeuGluSerAlaAspProValProAlaGlyThrAsp 2427
QY 578 -----AACTGGTGGCTAAAG 593
DB 2427 roValGluAlaGluPheTrpGluLeuValGluAsnThrAspLeuSerGlyLeuAlaAspG 2447
QY 594 GGCCTGGAGCTGTGATCCGACGCCATACCTCC----- 631
DB 2447 LuLeuGlyAlaAspAlaAlaLeuValGlyProAlaLeuProValLeuSerAlaTyrPA 2467
QY 632 -----AAAGCTCCCACTACCTACAGAGGAAACCAAGCAATTCACGTTAACT 686
DB 2467 rGArGArgSerArGArgGluCysSerThrValAspGlyTyrArg-----TyrArgValSerP 2485
QY 687 ACACCCAGACCTGGACAAAGTCATGCTGCAGTGAAGAAATGACGGTGTCTGTCA 746
DB 2485 heArGArgLeuThrAsp-----HisAlaAlaProGlyLeuAsnGlyLeuTrpLeuA 2502

```

```

QY 747 CTCTTTTCTGAGACTGGTAATGAGGAACAACACGG-----ATTAACTGAATT 800
DB 2502 laValLeuProAlaGlyLeuAlaAspGluGlnTrpAlaProCysValValGlyValLeuA 2522
QY 801 GTACTCAGAAGCTTTGATGACAGCTGTGATTTT-----CTTCCCGGACAAAC 851
DB 2522 laAlaHisGlyAlaValValArgValValGluLeuProValAspCysAspArgSerGlnA 2542
QY 852 AACCTTATCAGAAGACCGAAATCTGTCACTGGAGAAGCT-----TGCTTCTACATA 905
DB 2542 laAlaValArgGluLeuAlaGluGluLeuArgGlyGluGlnProAlaGlyValLeuSerMet 2562
QY 906 CTGAAATGGAGAGCTTATGC-----ACACTGATGAATCTGTCCCTG 950
DB 2562 euGlyLeuAlaProGlyCysHisProAlaHisProThrLeu-----SerAlaSerLeuA 2580
QY 951 CAACCAATGATGTCAATTAATAAGACACCTAAACTATCTCATATTCGCTTAGCCCTTG 1010
DB 2580 laThrThrValThrLeuGln-----AlaLeuG 2590
QY 1011 GGGTGGGAGAACCTTAGAGCTCAAGTCAAGTCAAGTCTGGCCCTGTGCTGTTCTGGGA 1070
DB 2590 Ty-----AspValAspValGlnAlaProLeuTrpCysAlaThrArgGly- 2604
QY 1071 GCAGCTGTCTGCAGGGTGTGAGCTGACCTTATCTACACAGGTGAGATGTCCATCATG 1130
DB 2605 --AlaValSerThrArgValThrAspProLeu-----ArgA 2616
QY 1131 ATACTTTGATGCTGCTCCCAAGATAAATGTCACTCTGTGAACACAGACACTG 1190
DB 2616 sprAlaGlyAlaGlnLeuTrpGlyLeuGlyValAlaAlaValGluLeuProArgA 2636
QY 1191 AACGAGCTTTCTTTCTGTGACCTTCGAGATATGCTGATCTCTGAGAAATTAATATA 1250
DB 2636 rGTrpGlyGlyLeuValAspLeuProGluGluLeuAspGluHisAlaLeuArGArgLeuA 2656
QY 1251 ATATATCTATCAGAGACTGACAGAGGAGCCCTTCAAGTG 1291
DB 2656 laGlyValLeuAlaGlnHisAspGluAspGluLeuAlaVal 2669

```

```

RESULT 6
US-09-934-899-4
: Sequence 4, Application US/09934899
: Patent No. US20020102697A1
: GENERAL INFORMATION:
: APPLICANT: Wang, Siqun
: APPLICANT: Wang, Tao
: APPLICANT: Kofias, Matheos
: APPLICANT: Odom, J. Martin
: APPLICANT: Ye, Rick
: TITLE OF INVENTION: Genes encoding exopolysaccharide production
: FILE REFERENCE: CL1633 US NA
: CURRENT APPLICATION NUMBER: US/09/934, 899
: CURRENT FILING DATE: 2001-08-22
: NUMBER OF SEQ ID NOS: 18
: SOFTWARE: Microsoft Office 97
: SEQ ID NO 4
: LENGTH: 473
: TYPE: PRT
: ORGANISM: Methylobionas 16a
US-09-934-899-4

```

```

Alignment Scores:
Pred. No.: 0.336      Length: 473
Score: 104.50      Matches: 62
Percent Similarity: 32.75%      Conservative: 31
Best Local Similarity: 21.83%      Mismatches: 88
Query Match: 3.75%      Indels: 103
DB: 10      Gaps: 13

```

US-09-745-506-74 (1-1553) x US-09-934-899-4 (1-473)

Db 425 AlaGlnValAsnGlyTTrpArgGlyAspThrAspLeuAsnArgArgIleGluHisAspLeu 444
Qy 683 AACTACACCCAA 694
Db 445 TyrTyrIleGln 448

RESULT 8
US-10-353-457-4
; Sequence 4, Application US/10353457
; Publication No. US20030148494A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Siqun
; APPLICANT: Wang, Tao
; APPLICANT: Koffas, Matheos
; APPLICANT: Odom, J. Martin
; APPLICANT: Ye, Rick
; TITLE OF INVENTION: Genes encoding exopolysaccharide production
; FILE REFERENCE: CL1633 US NA
; CURRENT APPLICATION NUMBER: US/10/353,457
; CURRENT FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: US/09/934,899
; PRIOR FILING DATE: 2001-08-22
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 4
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Methylobionas 16a
US-10-353-457-4

Alignment Scores:
Pred. No.: 0.336 Length: 473
Score: 104.50 Matches: 62
Percent Similarity: 32.75% Conservative: 31
Best Local Similarity: 21.83% Mismatches: 88
Query Match: 3.75% Indels: 103
Gaps: 13
DB: 12

US-09-745-506-74 (1-1553) x US-10-353-457-4 (1-473)

Qy 41 AGATTGGGTGAGAAAAGTCCCTGCCG-----CACGAGACACACGACACTAG 88
Db 202 ArgLeuGlyLysLeuSerAspLeuProArgLeuValSerArgGlnAlaValAspGluVal 221
Qy 89 TGGGACAGGGGCTCGACTGACGACTTAAGTGGCTGTGCTCGTTCGTTTCACTGCTCCG 148
Db 222 TrpValAlaIlePheProGlyValAspSerLeuAlaGluArgValGln----- 235
Qy 149 GAAAAGGCTGAGTGGACAGTGAATGAGCATAGTGCACCCACGACAGTCCGGTTT 208
Db 236 -----HisGluLeuArgHis-----LeuProValSerIleArgLeu 247
Qy 209 GTAGATTCCCTGATGTGCATTTCTCCCTTCCTTCATGATTTGAAGCTTCCTTTCT 268
Db 248 ValIleAspCysPheAlaIlePheLysGlnSerLysPheLeu----- 260
Qy 269 TCCTTGATGACTTGGATCCCTCTCCCTTCCTTCGCTGAGAGTGGGACAAATTGTGATTACTG 328
Db 261 SerLeuAspTrpValAlaIleLysProThrLeuAsp----- 272
Qy 339 GTGGAACCAAGCCACACATAGTACTTAATATACACTTCTTCGACCAATGACCTGACTGAG 388
Db 273 ValSerValSerProLeuHisGlyValAsnArgTyrIle-----Lys 286
Qy 389 GAAGTGAATGGAGAGTGTCTGCAAAAAGAGACCTCATTT----- 430
Db 287 GluIleGluAspArgLeuValAlaLeuLeuLeuLeuLeuIleSerProLeuMetLeu 306
Qy 431 -----CTCTCCATCATTCCGCTATCTTCCTCGACCCATGAAAGGCG 469
Db 307 ValIleAlaLeuGlyValLysLeuSerSerProGlyProValPheTyrLysGlnValArg 326
Qy 470 ATAACCTGGAACATGGAAGAGGCGCTGTG----- 502

Db 327 ValGlyTTrpAsnAsnArgLysPheThrMetLeuLysPheArgSerMetProValAspAla 346
Qy 503 -----ATCCGGGCTCTGGACAGACAGTCT-----GGT 529
Db 347 GluAlaLysThrGlyAlaValTrpAlaAspProGlyGluAsnArgAlaThrArgPheGly 366
Qy 530 ATCTACTCTCCATCATACAGCTATGATGCTGGCCGCCGACAGGCGTCAACAAGTGGTGGCT 589
Db 367 AlaPheLeuArgLysThrSerLeuAspGluLeuProGlnLeuIleAsn-----ValLeu 384
Qy 590 AAGGG-----CTTGAGCTTGTACTCCAGGCC-----ATACAT 625
Db 385 LysGlyAspMetSerLeuValGlyProArgProGluArgProAspPheValGluValPhe 404
Qy 626 CCTCCAAAGCTCCCACTAC----- 646
Db 405 LysAspGlnValProAsnTyrMetLysLysHisMetValLysAlaGlyIleThrGlyTrp 424
Qy 647 -----CCTACAGAGGGAACACGAGTACAGTATTCACAGTT 682
Db 425 AlaGlnValAsnGlyTTrpArgGlyAspThrAspLeuAsnArgArgIleGluHisAspLeu 444
Qy 683 AACTACACCCAA 694
Db 445 TyrTyrIleGln 448

RESULT 9
US-10-156-761-8383
; Sequence 8383, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRU
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8383
; LENGTH: 1052
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8383

Alignment Scores:
Pred. No.: 0.495 Length: 1052
Score: 104.50 Matches: 99
Percent Similarity: 33.26% Conservative: 57
Best Local Similarity: 21.11% Mismatches: 188
Query Match: 3.75% Indels: 125
Gaps: 20
DB: 15

US-09-745-506-74 (1-1553) x US-10-156-761-8383 (1-1052)

Qy 11 TCTTGTGCTGCAGACGACAGAGAAGAGAGATTGGGTCAAGAAAAGTCCCTGCCGCGAC 70
Db 362 SerTyrCysTrpLeuLysSerAlaLysProAsnIleGlyHisLeuAspAla----- 378
Qy 71 CAGAGACAGAGCGACATAGTGGGACAGGGTCTCGATCAGACTTAAGTACGTGCTGTCTCG 130
Db 379 -----AlaAlaGlyIleAlaGly 384
Qy 131 TGGTTTCACTGTCTCTGGAAGAGGCTGAGTGCATGAATGAGCATAGATGATGTC 190

```

Db      385 LeuilelysthrValleu-----SerleuLysAsnArgLysVal 397
QY      191 CCCAGCAGACGCGGTTT-----GTGATTTCCCTGATCGC 226
Db      398 ProProValValaAsnPhenArgArgProAsnProLysLeuAlaLeuAspSerSerProphe 417
QY      227 AATTCCTCCGCTCCCTTCATGATTTGAGGCT-----CTCCCTTCTCTCTGAT 277
Db      418 ArgValAlaThrGluLeuThrArgLeuGluGluLysArgLysProLeuLeuAlaSerValAsn 437
QY      278 GACTTTGGATCCCTGCTGTTGCGAGAGTTGGGCAATGTGGATTCGTGGTGGACCA 337
Db      438 -----SerLeuAlaMetGlyGlyThrAsnAlaHisValValLeuGluGlu 452
QY      338 AGCCACCA-----CATCTGTAAATACACTC 364
Db      453 AlaProProValArgSerGlyGlyAlaSerArgArgArgHisProVal----- 469
QY      365 TTCTGACCAATGACCTGACTGAGAGAGTATGAGAGGAGGTGCAAAAG----- 415
Db      470 ---LeuSerAlaLysSerGlyGluAlaLeuGluAspLeuSerGlnSerLeuGlyGln 488
QY      416 -----AAGCAGACCTCATTCCTCTCCATCCGCTATCTTCGGA 457
Db      489 TPAlaArgGluAsnProHisAlaAspValAlaAspValAlaHis----- 503
QY      458 CCCATGAGGCCATTAACCTGGACACATGAGAGAGCCGCTGGATCCGAGGCTCTGGAG 517
Db      504 -----ThrLeuAlaThrGlyArgArgGluLeuProLeuAlaArg----- 516
QY      518 AACAGAGTCGATCTACTCTCCAT-----ACAGCTTATGATGCTCGCC 565
Db      517 -----AlaLeuThrAlaHisAspLeuAspValAlaLysGlyLeuSerThr 532
QY      566 CAGGCGCTGACCAACTGGTTG---GCTAAGGCGCTTGGAGCTTACTCCAGGCCCAT 622
Db      533 ArgGlySerArgSerGlnArgGluAlaGlnAlaArgLysValArgThrAlaPheLeu 552
QY      623 CATCTTCCAAAGCTCCCACTACCTACCTACAGAGGGAACCAAGAGTAAATCAACGTT 682
Db      553 PheProGlyGlnGlyThrGlnLeuProAlaMetGlyAlaArgLeuAlaGlnGlyAspPro 572
QY      683 AACATACACCAAGACCTGAGCAAAAGTCACTGCTGACAGCAAA-----GGAATTGAC 733
Db      573 ValPheAlaAlaHisLeuAspArgValIleGlyLeuPheGlnGluArgAlaGlyValAsp 592
QY      734 GGTGTTCTGTCACCTTTTCTGCTAGAGCTGATAGAGCAACAACAGGATTAAT 793
Db      593 LeuLeuProValLeuAlaArgProAspLaserThrLeuGluGluAlaArgThrLeuThr 612
QY      794 ---CTGAATTGCTACAGAGGCTTTGATGCAAGGTGATGATTTCTTCCGGAACAA 850
Db      613 AlaThrGluGlyThrGlnProAlaLeuPheAlaValGluThrPalaLeuGlyArgThrLeu 632
QY      851 CAACCTTATCAGAAAGCGAAATTCCTGCTACCTGGAAGACCTTCTTCTCAATCTGGA 910
Db      633 MetAspTyr-----GlyValAlaArgProTyrAlaMetLeuGlyHisSer 946
QY      911 ATGGAGCGGTTA-----TGACACTGATGATTAATCTGCTCCGCAACCATGATTAAT 964
Db      647 ValGlyGluLeuValAlaAlaThrLeuGlyGlyValLeuAspLeuAlaProAlaValGlu 666
QY      965 CGAATAAAGACACCTTAAACTATTCATATTCGCTTACGCTTGGGCGGAGAAC 1024
Db      667 LeuValAlaArgArgGlyArgLeu-----MetSerGlnThr 678
QY      1025 TTAGAGTCTCAAGTCAAGGCTGAGCCCTGTGCTGCTTGGAGAGCGGTTCTGAG 1084
Db      679 ProGluGlyAlaMetLeuTyrValAsnLeuAlaGluGluAlaAlaLysLeuLeuAsp 698
QY      1085 GGTGTGAGGCTGACCTTACCTC-----ACA 1111

```

```

Db      699 AspValProGlyAspLeuThrLeuAlaAlaValAsnAlaAspGlnLeuValValSer 718
QY      1112 GGTGAGATGTCCTCATCATGATTAATCTTGGATGCTGCTCCCAAGAAATTAATGATCCTC 1171
Db      719 GlnAlaProGlnGluValGluGluLeu---AlaAlaArgLeuArgAlaAspGlyValSer 737
QY      1172 TGTGAACACACCAACACCTGAAACGAGGCTTCTTCTGACCTT----- 1213
Db      738 CysGlyArgLeuGluValThrArgAlaPheHisSerProLeuMetAspThrAlaAlaAsp 757
QY      1214 -----CGAGATATGCTGATTCAC 1234
Db      758 ThrPheArgGlnAlaAlaAspSerHis 766

RESULT 10
US-10-005-956-2
; Sequence 2, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 673
; TYPE: PRT
; ORGANISM: homo sapiens
US-10-005-956-2

Alignment Scores:
Pred. No.: 0.561 Length: 673
Score: 103.00 Matches: 98
Percent Similarity: 36.18% Conservative: 67
Best Local Similarity: 21.49% Mismatches: 159
Query Match: 3.69% Indels: 132
Gaps: 23

US-09-745-506-74 (1-1553) x US-10-005-956-2 (1-673)
QY      9 TATCTTGGTGGCGACAGAGCAGAGAGAGATTTGGTCAGAAAAGTGGCCGCGC 68
Db      81 TTTTGGTGGTGGCGACAGAGCAGAGAGAGATTTGGTCAGAAAAGTGGCCGCGC 92
QY      69 AACAGACACACGCGCATAGTGGAGAGGCGCTGCTGACTCAAGACTTAATGAGCTGTG--- 125
Db      93 ThrGlyPheThrGlnGlySerLeuGlyThrAlaValAlaThrMetLysLysAlaAlaValThr 112
QY      126 -----TCTGCTGTTTTCACCTGCTCGAAGAACGCTGGAAGTGGCAATGAGGC 179
Db      113 ThrAspSerArg--TyrThrPheGlnAlaGluArgGlnMetAspCysAsnThrGluLeu 132
QY      180 ATAGATGAGTCCCAACGACA-----GTCCGCTTGTGATGATTCCTGATCTGCAATTTCT 233
Db      132 TslYsGluValGlyThrThrProIleValThrThrPheLeuThrGluIleProAlaGlyG 152
QY      234 CCGGTTCTTCATGATGATTTGAAGGCTCTCTTCTCTCTGTAATGACTTTGCATCCCTCT 293
Db      152 LysGluValGlyPheAsp---ProPheLeuLeuSer----- 162
QY      294 CGTTTGTCTGAGAGTGGGACCAATGTGGATTAATCTGCTGGAACCAAGCCACCATTAAGT 353
Db      163 -----TlasPThrThrPheLysThrGlnAspLeuAlaLeuGlnGlySerAsnArgGlnLeu 181
QY      354 TAAATACACTCTTCTCTGACCAATGACCTGACTGAGAGAAAGTATGAGAGAGGTGCTGCAA 413

```



```

Db      181 alser-----ilethrtthrasnleu-----187
QY      414 AGAAGCAGACCTCATCTC---TCCTACCATCC-----CCTATCTTC 455
Db      188 -----ValaspleuValitrglysergluarproprovalproanglnproiletyra 206
QY      456 GACCCATGAAGGCATACCTGGACACATGGAAGAGCGCCGCGGATCCGGGCTGG 515
Db      206 lalenglnglnalaphethrlyserthrtrpglnlulysval-----220
QY      516 AGAACAGAGTCGGTATCTACTCTCTCATACACAGCTATGATGCTGCCGCCAGGGGCTC- 574
Db      221 -----serglvalargserglmeteglulyslsglnlulysvalprothralaval 238
QY      575 -----ACACACTGGTGGCTTAAAGGCTTGAAGCTTGACTCTCA 614
Db      238 euleuseralaleuglulthrAlatrlpleuPheasn-----250
QY      615 GGCCCATACATCTCTCCAAAGCTCCCAAGCTCCACACTACACAGGGAACACACAGTAGAAT 674
Db      251 -----leuargalaserasplleprotyrasnPro-----P 261
QY      675 TCACACTTAACCTAACACCCCAAGACCTGACAAAGTCACTGCTGCAGTGAAGAGTAATGACG 734
Db      261 hepethrlyserlythrleuLeuthrAsp-----Sers 272
QY      735 GTGTTCTCTGCTACTCTTTTCTGCTAGACACTGTATAGAGAACAAACAGATTATC 794
Db      272 erlletrglueuphealasnlyserArgPheaserseglulthrleuSerlytleuasn 292
QY      795 TGAATGTACTCAGAGGCTTGTGATCAGGTGTAGATTCT-----835
Db      292 erSerlyserthrglyPrometCysvalGlnlleglulasptryserglulvalargAspser 312
QY      836 -----CTTCCCGGAAACAACTTATC 860
Db      312 leglinalatyrserleuglyAspvalArgiletrpleglulthrserlythrmetyrg 332
QY      861 AGAAGCAGAAATCTCTGCTACCTGAGACAGCTTGTCTTCACTACTGGAATGGACGGT 920
Db      332 lytletrglumetlleproarglulys-----341
QY      921 TATGACACTGATCTGATCTGTCTCCGACACACATGATGATCGAATGAAAAAGACAC- 979
Db      342 -----leuvalthrAspThrlyserProvalmetethrlysalavalylasnsert 360
QY      980 -----CTAAACTATCTCATATTCCTTACGCTTGGGGTGGGAGA--- 1021
Db      360 ysglulglinalaleuLeulysalaserHlvalargAspAlaValAlleargTyl 380
QY      1022 -----ACCTTAGAGTCAAGTCAAAGTCGTGGCCCTGTGTGCTGTGGAGACAGC 1076
Db      380 euValitrgpleuglulysasnValProlysglythrvalAspglupheasergllyalglul 400
QY      1077 TTCTGAGGAGGTGTGGAGCTGACCTTACCTCACAGGTCAGATGTCCTCATCATGATCT 1136
Db      400 levalAspLysPhearglyglulglulnphesererglyproser---Pheglulthri 419
QY      1137 TGGATCTGCTCTCCCAAGGAATGAATGTCATCTCTGTGAACACAGCACTGA--- 1192
Db      419 leseralaser-----GlyleuasnAlaAlaValAlaHlstryserProcthrlysglul 437
QY      1193 -----CGAGGCTTCTTCTGACCTTCGAGATATGCTGATCT 1231
Db      437 euaSnarglyleuSerSerAspGlumetlyrleuLeuaspSer 451

```

```

RESULT 11
US-10-005-956-4
; Sequence 4, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company

```

```

; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005,956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251,015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263,678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273,037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 673
; TYPE: PRT
; ORGANISM: homo sapiens
; US-10-005-956-4

Alignment Scores:
Pred. No.: 0.561 length: 673
Score: 103.00 matches: 98
Percent Similarity: 36.18% conservative: 67
Best Local Similarity: 21.49% mismatches: 159
Query Match: 3.69% indels: 132
DB: 15 gaps: 23

US-09-745-506-74 (1-1553) x US-10-005-956-4 (1-673)
QY      9 TATCTGTGCTGCTCAGAGACACAGAGAGGAGATTGGTCAAGAAACTGCCCTGCCG 68
Db      81 Tylrlegly---GlnHlAspRgluarArgAla---Trple-----92
QY      69 ACAGAGACAGAGGCACTACTGGGACAGGGGCTCTGACTCAAGCTTAACGTGCTG--- 125
Db      93 ThrGlyPheThrlyserAlaGlyThrAlaValAlaValThrMetlyslsAlaAlaValTrp 112
QY      126 -----TCTGTGTTTCTCAGCTGCTCCGGAAGAGCCCTGAAGTGCACATGAATGAGC 179
Db      113 ThrAspserArg---TyrtrThrGlnAlaGlnlularglmetAspCysAsnTrpGlul 132
QY      180 ATAGATGAGTCCCCACGACA-----GTCCGTTTGTAGATTCCTGATTCGCAATTCCT 233
Db      132 lAsylglulValGlyThrThrProIllevalThrtrpleuLeuthrGlnlulProAlaGly 152
QY      234 CCCGTCCTCATGATGATTTGAAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 293
Db      152 lYargvalGlyPheasp---ProPheLeuLeuSer-----162
QY      294 CGTTTGTGAGAGTGTGGACAAATGTTGATTACTGTGTGAACCAAGCCACACATCTG 353
Db      163 -----lleAspThrtrpGlulserTyrAspLeuAlaLeuGlnlulysAsnArgGln 181
QY      354 TAAATACACTCTTCTGACCAATGACCTGACTGAGAGATGATGAGAGAGGTCTGCAAA 413
Db      181 alser-----ilethrtthrasnleu-----187
QY      414 AGAAGCAGACCTCATCTC---TCCTACCATCC-----CCTATCTTC 455
Db      188 -----ValaspleuValitrglysergluarproprovalproanglnproiletyra 206
QY      456 GACCCATGAAGGCATACCTGGACACATGGAAGAGCGCCGCGGATCCGGGCTGG 515
Db      206 lalenglnglnalaphethrlyserthrtrpglnlulysval-----220
QY      516 AGAACAGAGTCGGTATCTACTCTCTCATACACAGCTATGATGCTGCCGCCAGGGGCTC- 574
Db      221 -----serglvalargserglmeteglulyslsglnlulysvalprothralaval 238
QY      575 -----ACACACTGGTGGCTTAAAGGCTTGAAGCTTGACTCTCA 614
Db      238 euleuseralaleuglulthrAlatrlpleuPheasn-----250
QY      615 GGCCCATACATCTCTCCAAAGCTCCCAAGCTCCACACTACACAGGGAACACACAGTAGAAT 674

```


Db 332 lylletyrglumetileproarglulys----- 341
Qy 921 TATGACACTGATGATGTCTCCCGCAACCATGATGATGATAAAGACAC- 979
Db 342 -----leuvalthrpsprthrtyrserprovalmetethrlysalavalysasnsertl 360
Qy 980 -----CTAAACATATCATATTCGCTAGCCCTTGCGGGGAGAG- 1021
Db 360 yslglulinalaleuuleuylsalaserhlsvalragspalavalalvalleargtyrl 380
Qy 1022 -----ACCTTAGACTCTCAAGATCGTGGCCCTGTGCTGTGCTGAGCAGCG 1076
Db 380 euvaltrpreuulgulysasnservalprolysglythrvalasplupheserlglyalglul 400
Qy 1077 TTCTGACAGGTGTGAGCTGACCTTACCTCAGAGGTGATGATGCTCCATCATGATCTT 1136
Db 400 levalasplysphearglyglugluglnpheserterglproser---pheglutthrl 419
Qy 1137 TGGATGCTGCTCCCAAGAAATAATGTCATCCTGTGACACAGCAGCACTGAA- 1192
Db 419 leseralaser-----glyleuasnalaalaleualahlstryserprothrlysglul 437
Qy 1193 -----CGAGGCTTCTTCTGACCTTGACATATGCTGATTCCT 1231
Db 437 euasnarglylserseraspglumetlyrleuasnasper 451

RESULT 13

US-10-005-956-857
; Sequence 857, Application US/10005956
; Publication No. US20030113726A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
; FILE REFERENCE: D0053NP
; CURRENT APPLICATION NUMBER: US/10/005, 956
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/251, 015
; PRIOR FILING DATE: 2000-12-04
; PRIOR APPLICATION NUMBER: 60/263, 678
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/273, 037
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1579
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 857
; LENGTH: 673
; TYPE: prt
; ORGANISM: homo sapiens
US-10-005-956-857

Alignment Scores:

Pred. No.: 0.561 Length: 673
Score: 103.00 Matches: 98
Percent Similarity: 36.18% Conservative: 67
Best Local Similarity: 21.49% Mismatches: 159
Query Match: 3.69% Indels: 132
Gaps: 23

US-09-745-506-74 (1-1553) x US-10-005-956-857 (1-673)

Qy 9 TATCTGTGCTGTCAGAGGACAGACAGAGAGATGGTCAGAAAAGTCCCTGCCG 68
Db 81 Tyltlegly---glnhlsaspluaraglalga---Trrlle----- 92
Qy 69 ACCAGACGACAGCGACTAGTGGGACAGGGGCTCTGACTCAGACTTAAGTCTGTCG 125
Db 93 Thrhglyphtthrghlyseralaglythrvalavalvalrmetylsyalalvalttrp 112
Qy 126 -----TTCGTGCTGTTTTCACGCTGCTGGAAGGCCGGAAGTGCACACTGAATAGCG 179
Db 113 Thrapsrarg---tyrttrphtglnalagluarglumetaspysaantpgluleuh 132

Qy 180 ATAGATGAGTCCCGACAGACA-----GTCCGGTTGTAGATTCCGTGATGCAATTCTT 233
Db 132 lslsgluvalgllythrthrproillevalthrtrpleuenthrgulileproalglg 152
Qy 234 CCCGTCCTTCATGATGATGGAAGGCTTCCTTCTCTCTGTAATGACTTTCATCCCTCT 293
Db 152 lYArvalglYpheaap---ProPheleuenser----- 162
Qy 294 CGTTTCTGAGAGTTGGGACATGTTGGATTAATGATGATGACCAACCCACCATACG 353
Db 163 -----lleaspttrtpglusertryrpspleuallaleuunglysearasnarglnleuy 181
Qy 354 TAAATACACTCTCTCGACCAATGACCTGACAGAGAGATGAGAGAGGTCTGCATA 413
Db 181 alser-----llethrthrasnleu----- 187
Qy 414 AGAAGCAGACCTCATATCTC---TCCYACCATCCG-----CCTATCTTCC 455
Db 188 -----ValaspleuValtrpglysergluargrprobovalProanglnProilletyrA 206
Qy 456 GACCCATGAAGCGCATTAACCTGGAACACATGGAAGAGCGCCGTGGATCCGGCTCTGG 515
Db 206 lalenglnglualaphethrghlyserthrtrpelnulysval----- 220
Qy 516 AGAACAGAGTCGCTATCTCTCTCATACACAGCTATGATGCTGCGCCCGCCAGGCGTC- 574
Db 221 -----serglvalaryserglmeclnlyshlsnglnysvalprothrlalval 238
Qy 575 -----MACACTGCTGGCTTAAGGGCTTGAGCTTGACTTCCA 614
Db 238 euleuseralaleugluglugluthralatrpheuphasn----- 250
Qy 615 GGGCCATACACTCTTCCCAAGCTCCCACTACCTACAGGGAACCCAGCTAGAA 674
Db 251 -----leuargalasrleprotyrasnro-----p 261
Qy 675 TCACAGTAACTACACCCCAAGACCTGACCAAGATCATGTCGATGAAAGAAATGACG 724
Db 261 hepethrsertrythrleuethrasp-----Sers 272
Qy 735 GTGTTTCTGCTACTTCTTTTCTGTAAGCTGTAATGAGCAACACGATTAATC 794
Db 272 erlleargleuphealasnlyserarpheserterglutrhleuasn 292
Qy 795 TGAATGTACTCGAAGGCTTGATGACAGGTGATGATTT 835
Db 292 ersercythrghlyprometcyvalglnlleulnsplyrserglvalarapsert 312
Qy 836 -----CTTCCCGGACMAACAATTATC 860
Db 312 leglnaltrysertleuglyasprvalargllettrplegllythrsertrythmetlyrc 332
Qy 861 AGAAGACGGAATTCCTGCTACGTGAGAGCCTTGTCTTACATPACTGGAATGGACGGT 920
Db 332 lylletyrglumetileproarglulys----- 341
Qy 921 TATGACACAGTGAATGCTGCTCCGCAACCATGATTCGAATAAAGACAC- 979
Db 342 -----leuvalthrpsprthrtyrserprovalmetethrlysalavalysasnsertl 360
Qy 980 -----CTAAACATATCATATTCGCTAGCCCTTGCGGGGAGAG- 1021
Db 360 yslglulinalaleuuleuylsalaserhlsvalragspalavalalvalleargtyrl 380
Qy 1022 -----ACCTTAGACTCTCAAGATCGTGGCCCTGTGCTGTGCTGAGCAGCG 1076
Db 380 euvaltrpreuulgulysasnservalprolysglythrvalasplupheserlglyalglul 400
Qy 1077 TTCTGACAGGTGTGAGCTGACCTTACCTCAGAGGTGATGATGCTCCATCATGATCTT 1136
Db 400 levalasplysphearglyglugluglnpheserterglproser---pheglutthrl 419
Qy 1137 TGGATGCTGCTCCCAAGAAATAATGTCATCCTGTGTAACACAGCACTGAA- 1192

```

Db      419 IeserAlaser-----GlyLeuAsnAlaAlaLeuAlaHisTyrSerProThrLysGluL 437
QY      1193 -----CGAGGCTTTCTTTGACCTTCGAGATATGCTGATTC 1231
Db      437 euAsnArgLysLeuSerSerAspGluMetTyrLeuAspSer 451

RESULT 14
US-10-213-509-5
; Sequence 5, Application US/10213509
; Publication No. US20030054485A1
; GENERAL INFORMATION:
; APPLICANT: Weiss, Joseph
; APPLICANT: Scott, Matthew
; TITLE OF INVENTION: JELLY BELLY GENES AND THEIR USES
; FILE REFERENCE: STAN-232
; CURRENT APPLICATION NUMBER: US/10/213,509
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/311,720
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 4123
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-213-509-5

Alignment Scores:
Pred. No.:      1.51      Length:      4123
Score:          102.50    Matches:      106
Percent Similarity: 27.31% Conservative: 36
Best Local Similarity: 20.38% Mismatches: 157
Query Match:      3.72% Indels:      221
                   Gaps:      25

US-09-745-506-74 (1-1553) x US-10-213-509-5 (1-4123)
QY      1406 CCCTCGAGACACTCTCTGGAACACACACCTCCACCTGATCATGTTACAATTAAAGT 1347
Db      1333 ProAlaserThrLeuProGlyProSerPro-----GlySerLeuAsp 1346
QY      1346 TGGGATCCAGCTGATTTGTGAAGATGCTGATTCCTGATTTCTGCAATTATACCACCT 1287
Db      1347 ThrAlaserSer-----ProLeuAlaserAlaserProAlaPro 1359
QY      1286 GAAGAGGCTCCCTGACAGTCTCTGATAGATAATATTATCTTATTCACAAGTAGAAT 1227
Db      1360 ProCysGlyProPheGluPheArgCysGly----- 1369
QY      1226 CCAGCATATCTGGAAGGTCAGAAAGAAAGCTCTGTCAGTGTCTGTCACAGAGGA 1167
Db      1370 -----SerGlyGlu-----CysThrProArgGly 1377
QY      1166 TGACATTTATTCCTTGGGAACAGACATCCAAAGTATCATGATGGACATCTCACCTGCA 1107
Db      1378 -----TrrPArgCysAspGlnGluAspCysAlaAspGlySerAspGluArg--- 1393
QY      1106 GGTAAAGGTCAAGCTTCACACACCTGTCAGAACGC---TCTCCAGAACACAGACACAGAG 1050
Db      1394 GlyCysGlyGlyProCysAlaProHisAlaProCysAlaArgGlyProHisGys--- 1412
QY      1049 CCAGACTTTGACTTGAGACTCTAAGGTTCTCCCAAGGGGCTAAGCGAATATGAG 990
Db      1413 -----ValSerProGluGln 1417
QY      989 ATAGTTTAGGTGCTTTTATTCGATCATCATGTTGCCAGGAGACAGATTATCA 930
Db      1418 LeucYsaAspGlyVal-----ArgGlnCysProAsp 1427
QY      929 GTGTGCATAAACGTCCTTCATTCAGATGTAGAACGAAGGCTTCCAGTGACAGAAATT 870
Db      1428 GlySerAspGluGlyProAspAlaCysValGluAlaProAlaProProAlaMetArgGly 1447

```

```

QY      869 CCGTCTTGATTAAGTTGTTGTTCCGGAAAGAAATCTAACCACTGATCAAAAGCT 810
Db      1448 ProProGluGln-----AlaGlyGlyProThrSerSerArgAlaProSerProPro 1464
QY      809 TCTGAGTCAATTCAGATTATCCGTGTTTGTCTCTATACAGCTCTAGCAAGAAAG 750
Db      1465 SerPro-----ProGluAlaGlnGlyGlyArgLys 1475
QY      749 AAGTCAGAAACACCTGCAATTCCTT-----TCACTGACAGATGACTT 705
Db      1476 GlyGlnGluArgSerArgThrHisLeuThrValProAlaGlySerThrGlnLeuProLeu 1495
QY      704 TGTCCAGGCTTGGGTGATGTAACGTTGAATTACTGCGGTGCTTCCTGTGAAGGT 645
Db      1496 CysProGlyLeu-----PheProCys----- 1502
QY      644 AGTTGGAGCTTTGGAAGAGATGATGGCCCTGGAAGTACAAAGCTCAAGCCCTTAAAGCA 585
Db      1503 -----GlyValAlaPro 1506
QY      584 ACCAGTTGTGACCGCTGGGGCCGACGATCATAGCTGTATGAGAGAGATAGATACCGA 525
Db      1507 GlyLeuCysLeuThrPro-----GluGln 1514
QY      524 CTCTGTCTCCAGAGCCCGGATCACCA----- 498
Db      1515 LeuCysAspGlyLeuProAspCysProGlnGlyLeuAspGlyLeuAspCysGlyLeuLeu 1534
QY      497 -----GGCGGCTTCGATGCTGCTCCAGCTTACCGCTGCTATG 459
Db      1535 ProAlaLeuGlyGlyProAsnArgThrLeuProCysProGluTyrThrCysProAsn 1554
QY      458 -----GTGCGA-----AGATAGCGGATGGTGTAGAGAAATGAGTCTGCTCT 414
Db      1555 GlyThrCysIleGlyPheGlnLeuValCysAspGlyGlnProAspCysGlyArgProGly 1574
QY      413 TTTCAGACACCTCTCCATCTCTCTGACAGCTCATTTG 372
Db      1575 GlnValGlyProSerProGlnGlnGlnCysGlyAlaTyrProGlyProThrProThr 1594
QY      371 -----TCAGAGAGGTGATTTACAGATATG 345
Db      1595 GlyProCysSerArgThrCysGlyProThrPheGlnGlnArgSerArgArgCysSerPro 1614
QY      344 GTGGGCTTGTTCCACAGTAATCCACATTTGTCACAC----- 306
Db      1615 LeuGlyLeuLeu-----ValLeuGlnAsnCysProGlyProGlnHisGlnSerGlnAla 1632
QY      306 ----- 306
Db      1633 CysPheThrAlaAlaCysProValAspGlyLeuTrpSerThrTrpSerProTrpSerVal 1652
QY      305 ---TCTCAGCAAGAGAGGGATGCAAGTCAATTCAGAGAAAGAGAGGCTTCAAT 249
Db      1653 CysSerGluProCysArgGlyThrMetThrArgGlnArgGlnCysHisSerProGlnAsn 1672
QY      248 CCATTAAGAAAGGAGAAATTCAGATCAGAGGAATTAACAACCGAGCTGTCTGGGGA 189
Db      1673 -----GlyGlyArgThrCysAlaAla----- 1679
QY      188 CTCATCTATGCTCTATTTCAGTGGCCTTCAGGCTTTTCCAGAGCACTGAAAAACAG 129
Db      1680 -----LeuProGlyGlyLeuHisSerThr 1687
QY      128 AGACAGCAGCAAGTTAAGTCTGAGTCAGACCCCTGTCCACTAGAGGCTGTCTGCT 69
Db      1688 ArgGlnThrLys---ProCysProGlnAspGlyCysPro---AsnAlaThrCysSerGly 1705

RESULT 15
US-09-954-987B-6
; Sequence 6, Application US/09954987B
; Publication No. US20030104523A1

```

```

: GENERAL INFORMATION:
: APPLICANT: Stefan Bauer
: APPLICANT: Grayson B. Lipford
: APPLICANT: Hermann Wagner
: TITLE OF INVENTION: PROCESS FOR HIGH THROUGHPUT SCREENING OF
: FILE REFERENCE: C1041/7016 (AMS)
: CURRENT APPLICATION NUMBER: US/09/954,987B
: PRIOR APPLICATION NUMBER: US 60/233,035
: PRIOR FILING DATE: 2000-09-15
: PRIOR APPLICATION NUMBER: US 60/263,657
: PRIOR FILING DATE: 2001-01-23
: PRIOR APPLICATION NUMBER: US 60/291,726
: PRIOR FILING DATE: 2001-05-17
: PRIOR APPLICATION NUMBER: US 60/300,210
: PRIOR FILING DATE: 2001-06-22
: NUMBER OF SEQ ID NOS: 230
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 6
: LENGTH: 1032
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-954-987B-6

Alignment Scores:
Pred. No.: 1.93 Length: 1032
Score: 98.50 Matches: 100
Percent Similarity: 37.29% Conservative: 57
Best Local Similarity: 23.75% Mismatch: 137
Query Match: 3.53% Indels: 127
DB: 11 Gaps: 27

US-09-745-506-74 (1-1553) x US-09-954-987B-6 (1-1032)
QY 251 TTGAGGCTCTCTTCTTCTGAAAT-----GACTTTGCATCCCTCTCG 295
DB 336 LeuArgLysLeuAanLeuSerPheAsnTyrGlnLysArgValSerPheAlaHisLeuSer 355
QY 296 TTTCCTGAGAGTGGCAATGTGTGATTAAGTGTGAGACCAACCCACACATATCTGA 355
DB 356 LeuAlaProSerPheGlySerLeuValAlaLeuLysGlnLeuAsp-----Met 371
QY 356 AATCACTCTCTCCGACCAAT-----GACCTGAGTGAAGAGTG 394
DB 372 HisGlyIlePhePheArgSerLeuAspGlnThrThrLeuArgProLeuAlaArgLeuPro 391
QY 395 ATGGAGAGGTGCTGCAAAAGAGAGACCTCATCTCTCCATCCGACCTATCTTC 454
DB 392 MetLeuGlnThrLeuArgLeuGlnMetLeuAsnThrLeuAsnGlnAlaGlnLeuGlyIlePhe 411
QY 455 CGACCCATGAAGCCCATACCTGGAACACATGGAAGAGCCCTGTGATCCGGGCTCTG 514
DB 412 ArgAlaPheProGlyLeuArgTyr-----ValAspLeuSer 423
QY 515 GAGAACAGAGTGGTATCTACTCTCATACAGCC---TATGATGGTGGCCCGACGGC 571
DB 424 AspAsnArgIleSerGlyAlaSerGlnLeuThrAlaThrMetGlyGlnAlaAspGlyGly 443
QY 572 GTCAACAAGTGTGGCTAAAGG-----CTTGAGCTGTGTACTCCAGGCCCATACAT 625
DB 444 GlnLysValIlePheGlnProGlyAspLeuAlaProAlaProValAspThrProSerSer 463
QY 626 CTTTCCAAAGCTCCCACTACCCCTACAGAGGGAACACCGAGTAGAATTCAACGTTAAC 685
DB 464 GluAspPheArgProAsnCysSerThr-----LeuAsn 474
QY 686 TACACCAAGACGCTGGAAGATCATGTCTGACAGTAAGAAGATTGACGGTTTCTGTC 745
DB 475 PheThrLeuAspLeuSerArg-----AsnAsnLeuValIleThrValGlnPro 489
QY 746 ACTTCTTTTCTCTAGACTGTATGAGGAACAAACAGGATTAATCTTAATGTACT 805
DB 746 ACTTCTTTTCTCTAGACTGTATGAGGAACAAACAGGATTAATCTTAATGTACT 805

```

```

DB 490 GluMetPhe---AlaGlnLeuSerHisLeuGlnCysLeuArgLeuSerHisAsnCysIle 508
QY 806 CAGAACGCTTGG-----ATGCAGCTGCTGATTTT 835
DB 509 SerGlnAlaValaAnglySerGlnPheLeuProLeuThrGlyLeuGlnValLeuAsp--- 527
QY 836 CTTTCCCGGACAA---CAACTTTATCAGAAG-----ACGAAATTCTGCTACTG 883
DB 528 LeuSerArgAsnLysLeuAspLeuTyrHisGlnHisSerPheThrGlnLeuProArgLeu 547
QY 884 GAGAACGCTTGTCTTACATAC---GGAATGGACGGTTA 922
DB 548 GluAlaLeuAspLeuSerTyrAsnSerGlnProPheGlyMetGlnGlyValGly----- 565
QY 923 TGCACACAGATGATCATCTGCTCCCTGCACACATGATGATGCAATTAAGAACACTA 982
DB 566 -----HisAsnPheSerPheValAlaHisLeu---ArgThrLeuArgHisLeu 580
QY 983 AAATATCTCATATTCGCTTAGCCCTTGGGGTGGGAGAACCTTAGACTTCAAGTCAAA 1042
DB 581 SerLeuAlaHis-----AsnAsnIleHisSerGlnValSer 592
QY 1043 GTCGTGCCCTGTGTCTGCTGT-----TCTGGACAGCGCT--- 1078
DB 593 --GlnGlnLeuCysSerThrSerLeuArgAlaLeuAspPheSerGlyAsnAlaLeuGly 611
QY 1079 CTGCAGGCTGTGAGGCTGACCTTACCTGCACAGTGAAGTGAATGCCATGATATCTTG 1138
DB 612 HisMetTrpAlaGlnGlyAspLeuTyrLeu-----HisPhe----- 623
QY 1139 GATGCTGCTTCCCAAGAAATAAATCATCTCTGTGAACACAGCACATGAAAGAGC 1198
DB 624 -----PheGlnGlyLeuSerGlyLeuLe----- 631
QY 1199 TTTCTTGTGACCTTTCGAGATATGCTGATTTCTCACTGGAATATAGATTAATTTATC 1258
DB 632 -----TrpLeuAspLeuSer---GlnAsnArgLeuHisThrLeu 643
QY 1259 CTATCAGAGACTGACAGGAGC-----CCTCTCAGTGGGTATTAATTCAGAAACAT 1309
DB 644 LeuProGlnThrLeuArgAsnLeuProLysSerLeuGlnValLeuArgLeu----- 660
QY 1310 CAGGATTAACATTTCTCAAAATCAGCTG-----ATGCCCAACTTAAT 1354
DB 661 ArgAspAsnTyrLeuAlaPhePheLysTrpTrpSerLeuHisPheLeuProLysLeuGln 680
QY 1355 TTG 1357
DB 681 Val 681

```

Search completed: August 22, 2003, 14:29:06
 Job time : 110 secs

THIS PAGE BLANK (USPTO)